

SEQUENCE LISTING

<110> Unilever plc

Unilever NV

<120> Production of Antibodies

<130> T7060

<160> 67

<170> PatentIn version 3.0

<210> 1

<211> 440

<212> DNA

<213> Artificial

<220>

<223> VHH with peptide linker

<220>

<221> CDS

<222> (1)..(417)

<400> 1

cag	gtg	cag	ctg	cag	gag	tca	ggg	gga	gga	ttg	gtg	cag	gct	ggg	ggc	48
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
1			5						10					15		
tct	ctg	aga	ctc	tcc	tgt	gca	gcc	tcg	gga	cgc	gcc	acc	agt	ggt	cat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	His	
			20					25					30			
ggt	cac	tat	ggt	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	gag	cgt	144
Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	Arg	
		35				40					45					
gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggt	aaa	gag	aca	tgg	tat	aaa	192
Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	Lys	
	50				55				60							
gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	aag	act	240
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Thr	
65					70				75					80		

003727 924260

acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt 288
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336
 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 100 105 110

gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384
 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa 437
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 130 135

ttc 440

<210> 2

<211> 139

<212> PRT

<213> Artificial

<400> 2

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
 20 25 30

Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 35 40 45

Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 100 105 110

Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 130 135

008127 9242260

<210> 3
 <211> 11
 <212> PRT
 <213> Artificial

<220>
 <223> myc linker
 <400> 3

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

<210> 4
 <211> 471
 <212> DNA
 <213> Artificial

<220>
 <223> VHH with linker
 <220>
 <221> CDS
 <222> (1)..(459)

<400> 4
 cag gtg cag ctg cag cag tca ggg gga ggc ttg gtg cag gct ggg ggg 48
 Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15
 tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
 20 25 30
 cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc 144
 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
 35 40 45
 gca act att agt cct ggt ggt agc aca cac tat gta gac tcc gtg aag 192
 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80
 caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct 288
 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 gcc aag ggg agg ggg ctg cag gct atg cag tac tgg ggc cag ggg acc 336
 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr

008127 94450

100 105 110
 ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg 384
 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
 115 120 125
 gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc 432
 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
 130 135 140
 tca gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 471
 Ser Glu Glu Asp Leu Asn Gly Ala Ala
 145 150
 <210> 5
 <211> 153
 <212> PRT
 <213> Artificial
 <400> 5
 Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
 20 25 30
 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
 35 40 45
 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80
 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
 115 120 125
 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
 130 135 140
 Ser Glu Glu Asp Leu Asn Gly Ala Ala
 145 150

00872476.121800

<210> 6
 <211> 468
 <212> DNA
 <213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(456)

<400> 6
 cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg 48
 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15
 tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
 20 25 30
 gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc 144
 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
 35 40 45
 gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag 192
 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 65 70 75 80
 caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct 288
 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg 336
 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc 384
 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
 115 120 125
 gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca 432
 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
 130 135 140
 gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 468
 Glu Glu Asp Leu Asn Gly Ala Ala
 145 150

<210> 7

<211> 152

003727 924260

<213> Artificial

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
20 25 30

Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
35 40 45

Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Ala	Ala
		115					120					125			

Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
130 135 140

Glu Glu Asp Leu Asn Gly Ala Ala
145 150

<210> 8

<211> 462

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1) .. (450)

<400> 8
 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15

 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
 20 25 30

 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45

 gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 50 55 60

 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240
 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
 65 70 75 80

 acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt 288
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

 tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc 336
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

 gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat 384
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
 115 120 125

 cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 432
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

 gat ctg aat ggg gcc gca tagtaacaat tg 462
 Asp Leu Asn Gly Ala Ala
 145 150

<210> 9

<211> 150

<212> PRT

<213> Artificial

<400> 9

Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15

 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
 20 25 30

 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45

0977476 131500

Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
50 55 60

Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
115 120 125

His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
130 135 140

Asp Leu Asn Gly Ala Ala
145 150

<210> 10

<211> 471

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(459)

<400> 10

acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
20 25 30

agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
35 40 45

gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
50 55 60

gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240

008727 96426260

Asp 65	Ser	Val	Lys	Gly	Arg 70	Phe	Ala	Val	Ser	Arg 75	Asp	Tyr	Ala	Glu	Asn 80								
acg Thr	gtg Val	tat Tyr	ctg Leu	caa Gln 85	atg Met	aac Asn	agc Ser	ctg Leu	aaa Lys 90	cct Pro	gag Glu	gac Asp	acg Thr	gcc Ala 95	gtt Val	288							
tat Tyr	tac Tyr	tgt Cys	aac Asn 100	aca Thr	agg Arg	gcc Ala	tac Tyr	tgg Trp 105	ggc Gly	cag Gln	ggg Gly	acc Thr	cag Gln 110	gtc Val	acc Thr	336							
gtc Val	tcc Ser	tca Ser 115	gcg Ala	cac His	cac His	agc Ser	gaa Glu 120	gac Asp	ccc Pro	agc Ser	tcc Ser	gcg Ala 125	gcc Ala	gcc Ala	cat His	384							
cac His 130	cat His	cac His	cat His	cac His	ggg Gly	gcc Ala 135	gca Ala	gaa Glu	caa Gln	aaa Lys	ctc Leu 140	atc Ile	tca Ser	gaa Glu	gag Glu	432							
gat Asp 145	ctg Leu	aat Asn	agt Ser	gag Glu	aaa Lys 150	gat Asp	gag Glu	cta Leu	tgataacaat tg							471							
<210> 11																							
<211> 153																							
<212> PRT																							
<213> Artificial																							
<400> 11																							
Thr 1	Met	Ala	Gln	Val 5	Lys	Leu	Gln	Gln	Ser 10	Gly	Gly	Gly	Leu	Val 15	Gln								
Ala	Gly	Gly	Pro 20	Leu	Arg	Leu	Ser	Cys 25	Ala	Ala	Ser	Gly	Arg 30	Thr	Phe								
Ser	Asn	Tyr 35	Ala	Val	Gly	Trp	Phe 40	Arg	Gln	Ala	Pro	Gly 45	Lys	Glu	Arg								
Glu	Phe 50	Val	Ala	Ala	Ile	Ser 55	Arg	Asp	Gly	Gly	Arg 60	Thr	Tyr	Tyr	Ala								
Asp 65	Ser	Val	Lys	Gly	Arg 70	Phe	Ala	Val	Ser	Arg 75	Asp	Tyr	Ala	Glu	Asn 80								
Thr	Val	Tyr	Leu	Gln 85	Met	Asn	Ser	Leu	Lys 90	Pro	Glu	Asp	Thr	Ala 95	Val								
Tyr	Tyr	Cys	Asn 100	Thr	Arg	Ala	Tyr	Trp 105	Gly	Gln	Gly	Thr	Gln 110	Val	Thr								
Val	Ser	Ser 115	Ala	His	His	Ser	Glu 120	Asp	Pro	Ser	Ser	Ala 125	Ala	Ala	His								

His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

Asp Leu Asn Ser Glu Lys Asp Glu Leu
 145 150

<210> 12

<211> 38

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 12
 agctgcgatc gcaagcttgg taccgggaat tctctaga

38

<210> 13

<211> 42

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 13
 aatttctaga gaattcccg taccagctt gcttgcgac gc

42

<210> 14

<211> 31

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 14
 tcgacccatg gcccgctagc caattggagc t

31

<210> 15

<211> 23

<212> DNA

008727 "9244260

<213> Artificial

<220>

<223> synthetic insert

<400> 15

ccaattggct agcgggcat ggg

23

<210> 16

<211> 22

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 16

ccaccacga gggaacatcg tg

22

<210> 17

<211> 39

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 17

gaattcccat ggtttacact cgaggtcctc tccaaatga

39

<210> 18

<211> 189

<212> DNA

<213> Artificial

<220>

<223> PCR product

<400> 18

ccaccacga gggaacatcg tggaaaaaga agacgttcca accacgtctt caaagcaagt

60

ggattgatgt gatattcca ctgacgtaag ggatgacgca caatcccact atccttcgca

120

agacccttcc tttatataag gaagttcatt tcatttggag aggacctga gtgtaaacca

180

008737 944660

tggaattc

189

<210> 19

<211> 21

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 19

ccggcaacag gattcaatct t

21

<210> 20

<211> 40

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 20

agctccatgg gatttgttct cttttcaciaa ttgccttcac

40

<210> 21

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 21

ttcttcttgt ctctacactt ctcttattcc tagta

35

<210> 22

<211> 35

<212> DNA

<213> Artificial

00321"9242660

Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln Val
20 25 30

Gln Leu

<210> 29

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 29

gacatcccat ggcaagcatc a

21

<210> 30

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 30

aagcttggtta acagccctta a

21

<210> 31

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 31

agggctggtta acaaacttga t

21

<210> 32

<211> 44

<212> DNA

<213> Artificial

009727 92426260

<220>

<223> PCR primer

<400> 32

agactgctgc agctgcacct gctttccaca aacaatggta gctg

44

<210> 33

<211> 19

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 33

aattaaccct cactaaagg

19

<210> 34

<211> 254

<212> DNA

<213> Artificial

<220>

<223> GBSS leader

<220>

<221> CDS

<222> (3)..(254)

<400> 34

cc atg gca agc atc aca gct tca cac cac ttt gtg tca aga agc caa
 Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln
 1 5 10 15

47

act tca cta gac acc aaa tca acc ttg tca cag ata gga ctc agg aac
 Thr Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn
 20 25 30

95

cat act ctg act cac aat ggt tta agg gct gtt aac aaa ctt gat ggg
 His Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly
 35 40 45

143

ctc caa tca aga act aat act aag gta aca ccc aag atg gca tcc aga
 Leu Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg
 50 55 60

191

act gag acc aag aga cct gga tgc tca gct acc att gtt tgt gga aaa
 Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys
 65 70 75

239

008727 " 92426260

cag gtg cag ctg cag
Gln Val Gln Leu Gln
80

<210> 35

<211> 84

<212> PRT

<213> Artificial

<400> 35

Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln Thr
1 5 10 15

Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn His
20 25 30

Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly Leu
35 40 45

Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg Thr
50 55 60

Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys Gln
65 70 75 80

Val Gln Leu Gln

<210> 36

<211> 18

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 36
catgcaggtg cagctgca

<210> 37

<211> 10

<212> DNA

<213> Artificial

003746-1800

<220>

<223> synthetic insert

<400> 37
gctgcacctg

10

<210> 38

<211> 24

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 38
cgcaagaccc ttcctctata taag

24

<210> 39

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 39
gagctcgaat tcttattata gctcatcttt ctctgaattc agatcctctt ctgagatgag 60

<210> 40

<211> 26

<212> PRT

<213> Artificial

<220>

<223> linker

<400> 40

Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
1				5					10					15	

Gly	Gly	Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	.
			20					25		

00873460

<213> Artificial

<223> PCR primer

20

<213> Artificial

<223> PCR primer

19

<213> Artificial

<223> synthetic insert

30

<213> Artificial

<223> synthetic insert

<400> 44
ccaattggct agcgggccat gg

22

<210> 45

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 45
gatccacctc gagtgtaaac catggcccg

29

<210> 46

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 46
ctagcgggcc atggtttaca ctcgaggtg

29

<210> 47

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 47
attgcctacg gcagccgctg

20

<210> 48

<211> 51

<212> DNA

<213> Artificial

09737476 434900
008727 924269

<223> PCR primer

tccaaccaat tggtactatg cggccccatt cagatcctct tctgagatga g

51

<211> 25

<212> DNA

<213> Artificial

<223> sequencing primer

gtctgtctaa agtaaagtag atgcg

25

<210> 50

<211> 60

<212> DNA

<213> Artificial

<223> PCR primer

tccaaccaat tgttatcata gctcatcttt ctcactattc agatcctctt ctgagatgag

60

<210> 51

<211> 29

<212> DNA

<213> Artificial

<223> PCR primer

agtcccccat ggtacgtcct gtagaaacc

29

<210> 52

<211> 25

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 52

cgttttcgtc ggtaatcacc attcc

25

<210> 53

<211> 24

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 53

cgcaagaccc ttcctttata taag

24

<210> 54

<211> 1154

<212> DNA

<213> Artificial

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15

47

ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser
20 25 30

95

ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys
35 40 45

143

gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp
50 55 60

191

009343E-121800

tat	aaa	gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	239
Tyr	Lys	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	
65						70					75					
aag	act	acg	gtt	tat	ctg	caa	atg	aac	agc	ctg	aaa	cct	gaa	gat	acg	287
Lys	Thr	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	
80					85					90					95	
gcc	gtt	tat	tat	tgt	gcc	gct	cga	ccg	gtc	cgc	gtg	gat	gat	att	tcc	335
Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Pro	Val	Arg	Val	Asp	Asp	Ile	Ser	
				100					105					110		
ctg	ccg	gtt	ggg	ttt	gac	tac	tgg	ggc	cag	ggg	acc	cag	gtc	acc	gtc	383
Leu	Pro	Val	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	
			115					120					125			
tcc	tca	gaa	ccc	aag	aca	cca	aaa	cca	caa	cca	caa	cca	caa	cca	caa	431
Ser	Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	
		130					135					140				
cca	caa	ccc	aat	cct	aca	aca	gaa	tcc	aag	tgt	ccc	aaa	tgt	cca	gcc	479
Pro	Gln	Pro	Asn	Pro	Thr	Thr	Glu	Ser	Lys	Cys	Pro	Lys	Cys	Pro	Ala	
	145					150					155					
cct	gag	ctc	ctg	gga	ggg	ccc	tca	gtc	ttc	atc	ttc	ccc	ccg	aaa	ccc	527
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	
160					165					170					175	
aag	gac	gtc	ctc	tcc	att	tct	ggg	agg	ccc	gag	gtc	acg	tgc	gtt	gtg	575
Lys	Asp	Val	Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	
				180					185					190		
gta	gac	gtg	ggc	cag	gaa	gac	ccc	gag	gtc	agt	ttc	aac	tgg	tac	att	623
Val	Asp	Val	Gly	Gln	Glu	Asp	Pro	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	
			195					200					205			
gat	ggc	gca	gag	gtg	cga	acg	gcc	aac	acg	agg	cca	aaa	gag	gaa	cag	671
Asp	Gly	Ala	Glu	Val	Arg	Thr	Ala	Asn	Thr	Arg	Pro	Lys	Glu	Glu	Gln	
		210					215					220				
ttc	aac	agc	acg	tac	cgc	gtg	gtc	agc	gtc	ctg	ccc	atc	cag	cac	cag	719
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	
	225					230					235					
gac	tgg	ctg	acg	ggg	aaa	gag	ttc	aaa	tgc	aag	gtc	aac	aac	aaa	gct	767
Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	
240					245				250					255		
ctc	ccg	gcc	ccc	atc	gag	aag	acc	atc	tcc	aag	gcc	aaa	ggg	cag	acc	815
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	
				260					265					270		
cgg	gag	ccg	cag	gtg	tac	gcc	ctg	gcc	cca	cac	cgg	gaa	gag	ctg	gcc	863
Arg	Glu	Pro	Gln	Val	Tyr	Ala	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	
			275					280					285			
aag	gac	acc	gtg	agc	gta	acc	tgc	ctg	gtc	aaa	ggc	ttc	tac	cca	cct	911
Lys	Asp	Thr	Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Pro	
		290					295					300				
gat	atc	aac	gtt	gag	tgg	cag	agg	aac	ggt	cag	ccg	gag	tca	gag	ggc	959
Asp	Ile	Asn	Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	
	305					310					315					
acc	tac	gcc	acc	acg	cca	ccc	cag	ctg	gac	aac	gac	ggg	acc	tac	ttc	1007
Thr	Tyr	Ala	Thr	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	
320					325					330					335	

009737476 "121800

ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa 1055
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu
 340 345 350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365

cag aaa tcc atc acc cag tct tcg ggt aaa taa taagaattcg agctcgaa 1154
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 55

<211> 377

<212> PRT

<213> Artificial

<400> 55

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro
 130 135 140

Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160

Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175

009727426121800

Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
180 185 190

Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
195 200 205

Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
210 215 220

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
225 230 235 240

Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
245 250 255

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
260 265 270

Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
275 280 285

Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
290 295 300

Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
305 310 315 320

Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
325 330 335

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys
370 375

<210> 56

<211> 1172

<212> DNA

<213> Artificial

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

09237476 131800

cc	atg	gag	gtg	cag	ctg	cag	gag	tca	ggg	gga	gga	ttg	gtg	cag	gct	47
Met	Glu	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala		
1				5					10					15		
ggg	ggc	tct	ctg	aga	ctc	tcc	tgt	gca	gcc	tcg	gga	cgc	gcc	acc	agt	95
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	
				20					25					30		
ggt	cat	ggg	cac	tat	ggt	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	143
Gly	His	Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	
			35					40					45			
gag	cgt	gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggg	aaa	gag	aca	tgg	191
Glu	Arg	Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	
		50					55					60				
tat	aaa	gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	239
Tyr	Lys	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	
	65					70					75					
aag	act	acg	gtt	tat	ctg	caa	atg	aac	agc	ctg	aaa	cct	gaa	gat	acg	287
Lys	Thr	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	
	80				85					90					95	
gcc	gtt	tat	tat	tgt	gcc	gct	cga	ccg	gtc	cgc	gtg	gat	gat	att	tcc	335
Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Pro	Val	Arg	Val	Asp	Asp	Ile	Ser	
				100					105					110		
ctg	ccg	gtt	ggg	ttt	gac	tac	tgg	ggc	cag	ggg	acc	cag	gtc	acc	gtc	383
Leu	Pro	Val	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	
			115					120					125			
tcc	tca	gaa	ccc	aag	aca	cca	aaa	cca	caa	cca	caa	cca	caa	cca	caa	431
Ser	Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Gln	Pro	Gln	Pro	Gln	
		130					135					140				
cca	caa	ccc	aat	cct	aca	aca	gaa	tcc	aag	tgt	ccc	aaa	tgt	cca	gcc	479
Pro	Gln	Pro	Asn	Pro	Thr	Thr	Glu	Ser	Lys	Cys	Pro	Lys	Cys	Pro	Ala	
	145					150					155					
cct	gag	ctc	ctg	gga	ggg	ccc	tca	gtc	ttc	atc	ttc	ccc	ccg	aaa	ccc	527
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	
	160				165					170					175	
aag	gac	gtc	ctc	tcc	att	tct	ggg	agg	ccc	gag	gtc	acg	tgc	gtt	gtg	575
Lys	Asp	Val	Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	
				180					185					190		
gta	gac	gtg	ggc	cag	gaa	gac	ccc	gag	gtc	agt	ttc	aac	tgg	tac	att	623
Val	Asp	Val	Gly	Gln	Glu	Asp	Pro	Glu	Val	Ser	Phe	Asn	Trp	Tyr	Ile	
			195					200					205			
gat	ggc	gca	gag	gtg	cga	acg	gcc	aac	acg	agg	cca	aaa	gag	gaa	cag	671
Asp	Gly</															

gac Asp 240	tgg Trp	ctg Leu	acg Thr	ggg Gly	aaa Lys 245	gag Glu	ttc Phe	aaa Lys	tgc Cys	aag Lys 250	gtc Val	aac Asn	aac Asn	aaa Lys	gct Ala 255	767
ctc Leu	ccg Pro	gcc Ala	ccc Pro	atc Ile 260	gag Glu	aag Lys	acc Thr	atc Ile	tcc Ser 265	aag Lys	gcc Ala	aaa Lys	ggg Gly	cag Gln 270	acc Thr	815
cgg Arg	gag Glu	ccg Pro	cag Gln 275	gtg Val	tac Tyr	gcc Ala	ctg Leu	gcc Ala 280	cca Pro	cac His	cgg Arg	gaa Glu	gag Glu 285	ctg Leu	gcc Ala	863
aag Lys	gac Asp	acc Thr 290	gtg Val	agc Ser	gta Val	acc Thr	tgc Cys 295	ctg Leu	gtc Val	aaa Lys	ggc Gly	ttc Phe 300	tac Tyr	cca Pro	cct Pro	911
gat Asp	atc Ile 305	aac Asn	gtt Val	gag Glu	tgg Trp 310	cag Gln	agg Arg	aac Asn	ggt Gly	cag Gln 315	ccg Pro	gag Glu	tca Ser	gag Glu	ggc Gly	959
acc Thr 320	tac Tyr	gcc Ala	acc Thr	acg Thr	cca Pro 325	ccc Pro	cag Gln	ctg Leu	gac Asp	aac Asn 330	gac Asp	ggg Gly	acc Thr	tac Tyr	ttc Phe 335	1007
ctc Leu	tac Tyr	agc Ser	aag Lys	ctc Leu 340	tcg Ser	gtg Val	gga Gly	aag Lys	aac Asn 345	acg Thr	tgg Trp	cag Gln	cgg Arg	gga Gly 350	gaa Glu	1055
acc Thr	ttc Phe	acc Thr	tgt Cys 355	gtg Val	gtg Val	atg Met	cac His	gag Glu 360	gcc Ala	ctg Leu	cac His	aac Asn	cac His 365	tac Tyr	acc Thr	1103
cag Gln	aaa Lys	tcc Ser 370	atc Ile	acc Thr	cag Gln	tct Ser	tcg Ser 375	ggt Gly	aaa Lys	tct Ser	gag Glu	aaa Lys 380	gat Asp	gag Glu	cta Leu	1151
taa taagaattcg agctcgaa																1172
<210> 57																
<211> 383																
<212> PRT																
<213> Artificial																
<400> 57																
Met 1	Glu	Val	Gln	Leu 5	Gln	Glu	Ser	Gly	Gly 10	Gly	Leu	Val	Gln	Ala 15	Gly	
Gly	Ser	Leu	Arg 20	Leu	Ser	Cys	Ala	Ala 25	Ser	Gly	Arg	Ala	Thr 30	Ser	Gly	
His	Gly	His 35	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	
Arg	Glu 50	Phe	Val	Ala	Ala	Ile 55	Arg	Trp	Ser	Gly	Lys 60	Glu	Thr	Trp	Tyr	

Lys 65	Asp	Ser	Val	Lys	Gly 70	Arg	Phe	Thr	Ile	Ser 75	Arg	Asp	Asn	Ala	Lys 80
Thr	Thr	Val	Tyr	Leu 85	Gln	Met	Asn	Ser	Leu 90	Lys	Pro	Glu	Asp	Thr 95	Ala
Val	Tyr	Tyr	Cys 100	Ala	Ala	Arg	Pro	Val 105	Arg	Val	Asp	Asp	Ile 110	Ser	Leu
Pro	Val	Gly 115	Phe	Asp	Tyr	Trp	Gly 120	Gln	Gly	Thr	Gln	Val 125	Thr	Val	Ser
Ser	Glu 130	Pro	Lys	Thr	Pro	Lys 135	Pro	Gln	Pro	Gln	Pro 140	Gln	Pro	Gln	Pro
Gln 145	Pro	Asn	Pro	Thr	Thr 150	Glu	Ser	Lys	Cys	Pro 155	Lys	Cys	Pro	Ala	Pro 160
Glu	Leu	Leu	Gly	Gly 165	Pro	Ser	Val	Phe	Ile 170	Phe	Pro	Pro	Lys	Pro 175	Lys
Asp	Val	Leu	Ser 180	Ile	Ser	Gly	Arg	Pro 185	Glu	Val	Thr	Cys	Val 190	Val	Val
Asp	Val	Gly 195	Gln	Glu	Asp	Pro	Glu 200	Val	Ser	Phe	Asn	Trp 205	Tyr	Ile	Asp
Gly 210	Ala	Glu	Val	Arg	Thr	Ala 215	Asn	Thr	Arg	Pro	Lys 220	Glu	Glu	Gln	Phe
Asn 225	Ser	Thr	Tyr	Arg	Val 230	Val	Ser	Val	Leu	Pro 235	Ile	Gln	His	Gln	Asp 240
Trp	Leu	Thr	Gly	Lys 245	Glu	Phe	Lys	Cys	Lys 250	Val	Asn	Asn	Lys	Ala 255	Leu
Pro	Ala	Pro	Ile 260	Glu	Lys	Thr	Ile	Ser 265	Lys	Ala	Lys	Gly	Gln 270	Thr	Arg
Glu	Pro	Gln 275	Val	Tyr	Ala	Leu	Ala 280	Pro	His	Arg	Glu	Glu 285	Leu	Ala	Lys
Asp	Thr 290	Val	Ser	Val	Thr	Cys 295	Leu	Val	Lys	Gly	Phe 300	Tyr	Pro	Pro	Asp
Ile 305	Asn	Val	Glu	Trp	Gln 310	Arg	Asn	Gly	Gln	Pro 315	Glu	Ser	Glu	Gly	Thr 320
Tyr	Ala	Thr	Thr	Pro 325	Pro	Gln	Leu	Asp	Asn 330	Asp	Gly	Thr	Tyr	Phe 335	Leu

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu
370 375 380

<210> 58

<211> 31

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<223> PCR primer

<400> 58

aggggaccca ggtcacgcgc tcctcagaac c

31

<210> 59

<211> 37

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 59

gagctttgtt gttgaccttg catttgaact ctttccc

37

<210> 60

<211> 26

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 60

caaatgcaag gtcaacaaca aagctc

26

<210> 61

<211> 42

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 61

ttcgagctcg aattcttatt atttaccoga agactgggtg at

42

<210> 62

<211> 27

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 62

ctgaggagac ggtgacctgg gtccct

27

<210> 63

<211> 46

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 63

agcccctgag ctctctgggag ggccctcagt cttcatcttc ccccg

46

<210> 64

<211> 61

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 64

ttcgagctcg aattcttatt atttaccoga agactgggtg atggatttct ggggtgtagtg

60

008727 944260

<210> 65

<211> 79

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 65

ttcgagctcg aattcttatt atagctcatc tttctcagat ttacccgaag actgggtgat 60

ggatttctgg gtgtagtgg 79

<210> 66

<211> 461

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (3)..(449)

<400> 66

cc atg gcc cag gtg cag ctg cag gag tct ggg gga ggc ttg gtg cag 47
Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln
1 5 10 15

gct ggg ggg tct ctg agg ctc tcc tgt gca gcc tct gga agc att ttc 95
Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe
20 25 30

aga cgt ccg cat atg ggt tgg ttc cgc cag gct cca ggg cag gag cgc 143
Arg Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg
35 40 45

gag ttg gtc gca ctg att tct gcg ggt ggt cgt aca tgg tat gca gac 191
Glu Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp
50 55 60

tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg 239
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
65 70 75

ctg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat 287

008727 344660

Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr		
80					85					90					95		
tac	tgt	act	gcc	ggg	ggg	tcg	tac	tgg	ggc	cag	ggg	acc	cag	gtc	acc	335	
Tyr	Cys	Thr	Ala	Gly	Gly	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr		
				100					105					110			
gtc	gcc	tca	gaa	ccc	aag	aca	cca	aaa	cca	caa	cca	gcg	gcc	gcc	cat	383	
Val	Ala	Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Ala	Ala	Ala	His		
				115				120					125				
cac	cat	cac	cat	cac	ggg	gcc	gca	gaa	caa	aaa	ctc	atc	tca	gaa	gag	431	
His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu		
				130				135					140				
gat	ctg	aat	ggg	gcc	gca	tagtaacaat	tg									461	
Asp	Leu	Asn	Gly	Ala	Ala												
				145													
<210>	67																
<211>	149																
<212>	PRT																
<213>	Artificial																
<400>	67																
Met	Ala	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala		
1				5					10					15			
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Ser	Ile	Phe	Arg		
			20					25					30				
Arg	Pro	His	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Gln	Glu	Arg	Glu		
		35					40					45					
Leu	Val	Ala	Leu	Ile	Ser	Ala	Gly	Gly	Arg	Thr	Trp	Tyr	Ala	Asp	Ser		
	50					55					60						
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu		
65					70				75						80		
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr		
				85					90					95			
Cys	Thr	Ala	Gly	Gly	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val		
			100					105					110				
Ala	Ser	Glu	Pro	Lys	Thr	Pro	Lys	Pro	Gln	Pro	Ala	Ala	Ala	His	His		
			115				120					125					
His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp		
	130					135					140						

Leu Asn Gly Ala Ala
145

00347 924260